

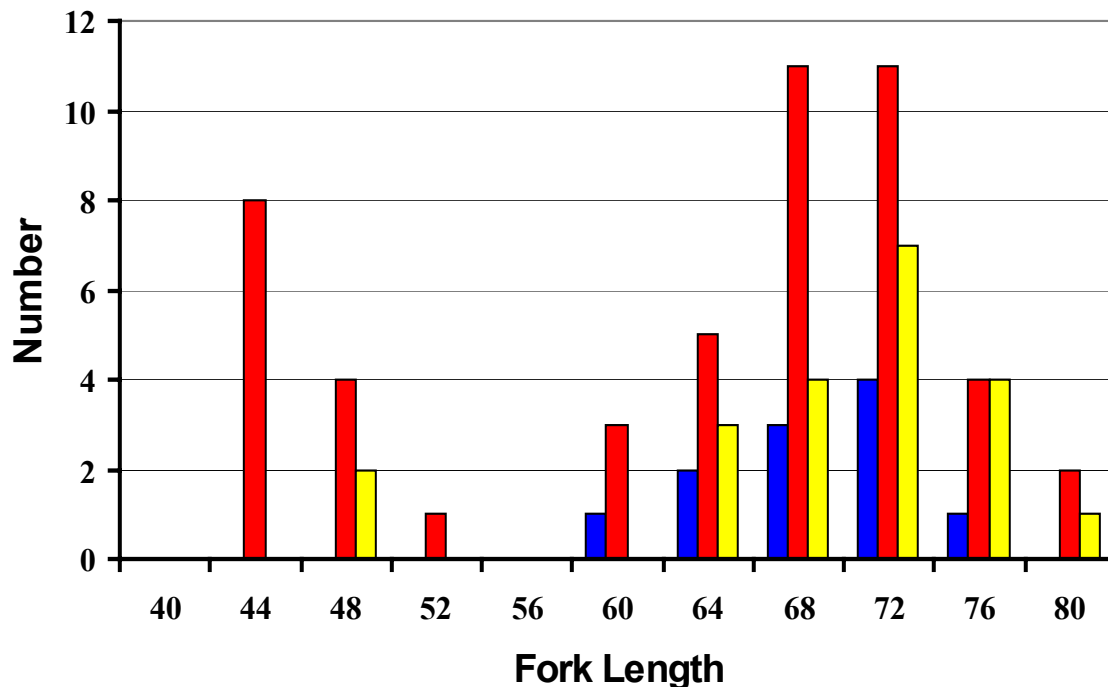
highly significant ( $F_{ST} = 0.036$ ,  $P < 0.00$ ). Upper Fork samples were the most heterogeneous and were removed. The  $F_{ST}$  for the remaining sample sites was 0.0191 and still significant ( $P < 0.030$ ). The further removal of RM 4.9 samples (SCY99up) yielded a homogenous population consisting of RM 2.55, RM 3.55, Big and Mill Creek samples (SCY99low, Table 2). Six out of twenty-one loci-pairs showed significant LD in the SCY99low population. The adjusted SCY99low population consisted of 12 unrelated individuals, and seven sibling groups, in most cases consisting of six to eight siblings per group (Table 4). After family adjustment, SCY99low was not homogenous with SCY99up, but the LD value was reduced to 3/21 significant pair associations.

## Results

### Genetic diversity within California Coastal Coho

Preliminary analyses of the genetic data suggested widespread departures from random mating expectations, as measured by tests of single-locus and multi-loci equilibria (2001 annual report). Although many of these deviations were observed in juvenile population samples, which are expected to deviate from random mating expectations, many samples of adults also appeared to depart from random mating equilibrium. First, we investigate the possibility that departures from random mating equilibrium within adult samples might have resulted from artificial admixture of fish from genetically different subpopulations.

The 1997 sample of 81 adults from the Klamath River Iron Gate Hatchery illustrates the Wahlund effect.  $F_{IS}$  for this sample is 0.076, a value that is attained in none of the 500 permutations of the alleles among individuals (*i.e.*  $P = 0.0$ ), and seven of 21 pairwise LD tests are significant at the 5% level. The distribution of fork lengths in the KIGHA97 sample shows a clear separation into jacks (males less than 56cm FL) and older adults (Fig. 2). The sample can also be subdivided by the presence and kind of mark (no mark, which could be either wild or



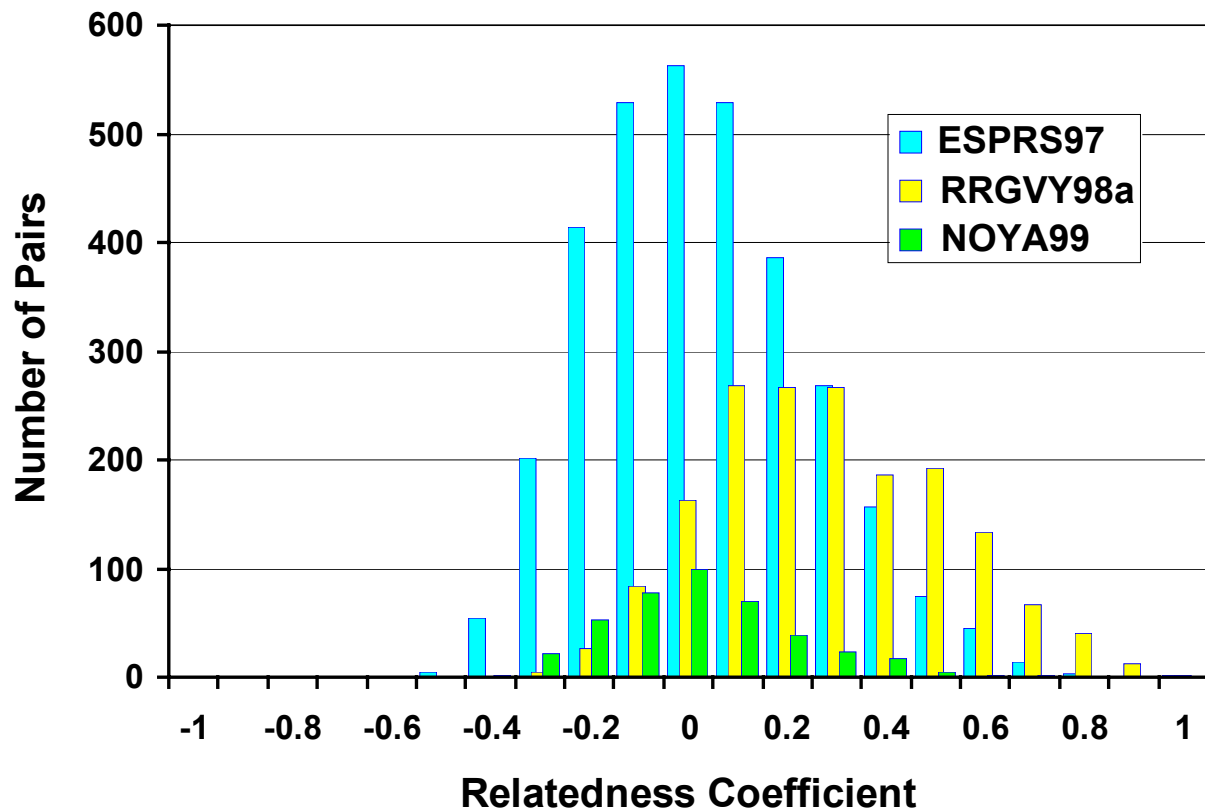
**Fig. 2.** Distribution, by fork length (cm) and mark, of adult coho salmon sampled from returns to the Iron Gate Hatchery, Klamath River, in 1997; blue bars are adipose fin clipped (Rogue River hatchery mark), red bars are left maxillary notched (the IGH mark), yellow bars are unmarked fish (wild or hatchery).

**Table 3.** Deviations from random mating genotypic proportions, by locus (\*,  $P < 0.05$ ; \*\*,  $P < 0.01$ ; \*\*\*,  $P < 0.001$ ) and over all loci ( $F_{IS}$ ,  $P$ ), and proportion of loci pairs showing linkage disequilibrium (LD) for 49 samples of coho salmon. NA indicates sample not analyzed because too few individuals were amplified successfully, or the locus was insufficiently polymorphic.

Population	N	<i>Ots-103</i>	<i>Ots-2</i>	<i>Iso-Ots2</i>	<i>Ots-3</i>	<i>One-13</i>	<i>P-53</i>	<i>Oki-1</i>	$F_{IS}$	$P$	LD
KIGHA97a	11								0.009	0.470	2/21
KIGHA97j	15			*					0.019	0.326	4/21
KIGHA97ll	36		*	**		*			0.073	0.012	3/21
KIGHA97nl	19								0.089	0.010	1/21
TRHA97s	17								0.024	0.276	2/21
TRHA97l	77	***		***				*	0.062	0.000	4/21
LRS00-1	85	***		***	***		**		0.080	0.000	9/21
LRS00-2	11			**					-0.014	0.668	6/21
EHOLA97	16	*							0.064	0.132	3/21
EREDS97	92		*	**					0.058	0.000	2/21
EREDA98	22	***							0.056	0.066	2/21
ESPRS99	34								-0.020	0.720	4/21
MATS98-1	73						*	*	0.030	0.112	7/21
MATS98-2	21					*			0.054	0.850	3/21
PUDY98h	32	*					*		0.068	0.022	5/21
PUDY98k	43	**	*						0.070	0.012	9/21
NOYA97	44				**			*	0.064	0.012	1/21
NOYA99	43	*		*					0.076	0.010	1/21
ALBA98	22					***		*	-0.012	0.642	6/21
ALBY98	18						*	*	-0.023	0.706	3/21
RRHA95	33	**							0.057	0.018	3/21
RRHA96	25						*		-0.046	0.914	4/21
RRHY97	7						*		0.120	0.060	5/21
RRGVY97	8		NA					**	-0.032	0.588	0/19
RRGVY98a	70	***	*	***		**	*	***	-0.047	0.978	15/21
RRGVY98b	58	***	*	***		*	*	***	0.019	0.202	15/21
RRGVY00	8		NA					*	-0.257	1.000	0/15
LAGA96	8							NA	-0.062	0.734	0/15
LAGA97	7								0.052	0.194	2/21
LDGA96	9								0.165	0.012	0/21
LDGA97	10							*	0.086	0.106	2/21
LSGA96	5								0.138	0.096	0/21
LSGA97	61								-0.014	0.718	4/21
LSGY98	12								-0.062	0.870	1/21
LSGAA96	25								0.000	0.538	0/21
LSGAA97	3								-0.042	0.672	0/21
LSGAY98	21						*	*	0.000	0.442	7/21
OLEA96	70				***			*	0.105	0.006	6/21
OLEA97	34				*		*	*	-0.010	0.610	3/21
OLEY98	88		*	**					-0.010	0.560	5/21
RWMA97	15	**		**	NA				0.113	0.090	0/18
RWMY98	24	*							-0.002	0.480	0/21
WADY99low	42	**		**	***				0.011	0.356	7/21
WADY99up	17						*		-0.085	0.900	2/21
SCA95	41								-0.051	0.958	5/21
SCA97	57	*		*	**				-0.047	0.966	15/21
SCA98	38	***		*	*	*	**	*	0.099	0.010	11/21
SCY99low	40								-0.028	0.780	7/21
SCY99up	20								-0.030	0.690	2/21

unmarked hatchery fish; left maxillary, which are from the IGH; adipose fin, which are likely from a Rogue River hatchery). For further analysis, the KIGHA97 sample is subdivided into three subsamples of adults greater than 56cm fork length differentiated by marks (adipose, left maxillary marks, no marks) and a jack subsample comprised of 13 left maxillary marked and 2 unmarked fish.  $F_{IS}$  is non-significant in two of the four subsamples but remains significant in the KIGHA97ll (left mark, large) and KIGHA97nl (no mark, large) subsamples; LD is reduced to low levels in two of the subsamples but remains moderately large, four and three of 21 pairwise comparisons, for the KIGHA97j (jacks) and KIGHA97ll subsamples, respectively (Table 3). There is significant variance ( $F_{ST}$ ) in all but one of the six pairwise comparisons among the four subsamples (see Table 6), suggesting that the original sample was an admixture of samples from genetically differentiated subpopulations. Similar adjustments for Wahlund effect were made in the Trinity River Hatchery 1997 adult sample and in the course of adjusting several of the juvenile samples (Table 2, “Criteria” column).

To investigate further the genetic characteristics of samples, we also dropped small samples that could not be combined with other samples in preliminary tests of homogeneity (*i.e.* PUDY98u, RRDS97, RRDS98, RRM98, Table 2), as well as those individuals in juvenile samples with insufficient data for testing relatedness. Of the 1745 samples in Table 2, we were left with 1587



**Fig. 3.** Relatedness coefficients calculated for all pairwise comparisons among individuals in three samples of coho salmon. The coefficient should have a mean of zero for unrelated individuals. The distribution for the Eel River has a mode at zero (n=3240) but is skewed towards pairs with coefficients above 0.5, the expected relatedness of full-sib pairs. Relatedness of Russian River Green Valley juveniles (n=1711) appears consistent with many full- and half-sib relationships. Even the distribution for Noyo River adults (n=406) is skewed towards high relatedness.

individuals in 49 populations for our initial analyses (Table 3). Of the 27 adult samples in Table 3, 9 or 33% have significant  $F_{IS}$  ( $P < 0.05$ ) and 9 or 33% have more than three significant pairwise LD tests. All three Scott Creek adult samples have high levels of LD; two have significant excesses and one has a significant deficiency of heterozygotes. By contrast, of the 22 juvenile samples in Table 3, only 4 or 18% have significant  $F_{IS}$ , but 13 or 59% have more than three significant pairwise LD tests. High levels of LD and relatedness, such as these are atypical for Pacific salmon populations (*cf* Bartley et al 1992a, b). Juvenile samples with high LD and the Scott Creek adult samples are adjusted for the effects of family structure.

Family structure is evidently strong in the RRGV98 samples, which have very high levels of linkage disequilibrium (15 of 21 loci-combinations) and, in the RRGV98a sample at least, a significant excess of heterozygotes (Table 3). More than 40% of the pairwise tests of the full-sib hypothesis in the RRGV98a sample are above the  $\alpha=0.01$  level of significance. SIBLINGS is unable, however, to form kinship groups out of the total sample, owing to the apparent complexity of family structure and the large number of discard permutations that has to be checked. We made the problem tractable for SIBLINGS by first subdividing the sample according to the degree of allele sharing among individuals. After determining kinship and sibling groups for the two major branches on the Neighbor-Joining tree (Fig. 4), we find that only 9 individuals are unrelated (the red branches on Fig. 4) and that the rest of the sample can be replaced by 16 sets of full-sib parents and 1 shared parent (Table 4). We similarly adjusted the RRGV98b sample, which was collected only three months later than the RRGV98a

**Table 4.** Samples adjusted for family structure. Min sib size is a SIBLINGS variable; UNR, unrelated; N, initial sample size; Nw, samples with sufficient data; NF, final sample size.

Population	N	Nw	Min sib size	Number of sibs per group					N	# UNR	# Parents	# Shared Parents	NF
				2	3	4	5	6					
LRS00-1	85	83	3	0	18	4	1	0	0	28	42	2	72
LRS00-2	11	11	3	0	2	0	0	0	0	5	4	0	9
EREDS97	92	89	4	0	0	11	1	1	0	52	24	1	77
ESPRS99	34	34	3	0	6	3	0	0	0	12	18	0	30
MATS98-1	73	73	3	0	0	0	0	0	0	27	0	0	27
MATS98-2	21	21	-	-	-	-	-	-	-	21	0	0	21
PUDY98h	32	32	3	NA	NA	NA	NA	NA	NA	21	0	0	21
PUDY98k	43	43	3	NA	NA	NA	NA	NA	NA	23	0	0	23
ALBY98	18	18	3	0	2	0	0	0	0	12	4	0	16
RRHY97	7	7	2	1	0	0	0	0	0	5	2	0	7
RRGV98a	67	59	2-3	3	4	2	0	0	25	9	16	1	25
RRGV98b	61	61	3	0	11	4	1	0	15, 8	8	23	8	39
LSGAY98	21	21	2	1	0	0	0	0	0	13	4	0	17
OLEY98	88	88	3	0	4	5	0	0	8	53	18	1	72
WADY99low	42	42	3	0	2	5	0	0	7	15	16	0	31
WADY99up	17	17	-	-	-	-	-	-	-	17	0	0	17
SCA95	41	41	2	10	0	1	0	0	0	17	22	0	39
SCA97	57	57	2	4	9	1	0	0	0	16	24	2	42
SCA98	38	38	2	3	5	0	0	1	0	5	18	0	23
SCY99low	40	40	4	0	0	1	0	5	8	12	8	3	23
SCY99up	20	20	-	-	-	-	-	-	-	20	0	0	20
Totals:	908	903											652

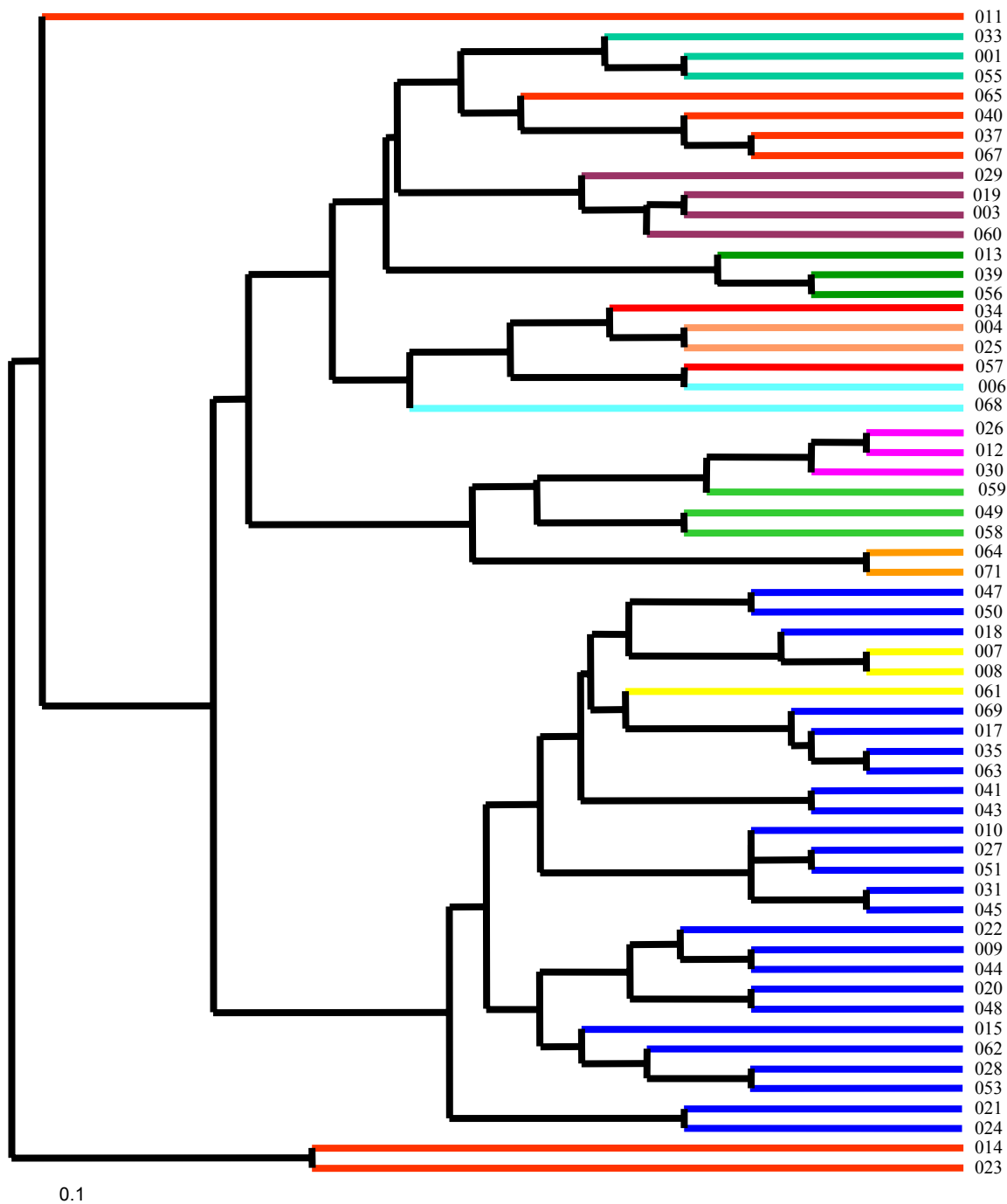
sample and likely contains the same families. Owing to the complexity of family structures in these two samples, however, we did not attempt to combine them but left them separate for further analyses of geographic pattern. Substantial adjustments for family structure were made to 16 other juvenile samples besides the RRGVY98 samples and to the three Scott Creek adult samples (Table 4). These adjustments result in a net loss of 257 individuals, owing to the discarding of full sibs and their replacement by reconstructed parents. Juvenile samples from the Mattole River and Pudding Creek could not be satisfactorily adjusted; only unrelated individuals from these samples are used in further analyses.

One of the full-sib families revealed in the RRGVY98a sample comprises 25 individuals (blue branches in Fig. 3). This family provides evidence for the Mendelian inheritance of the microsatellite DNA markers in coho salmon (Table 5). Moreover, knowing the distribution of

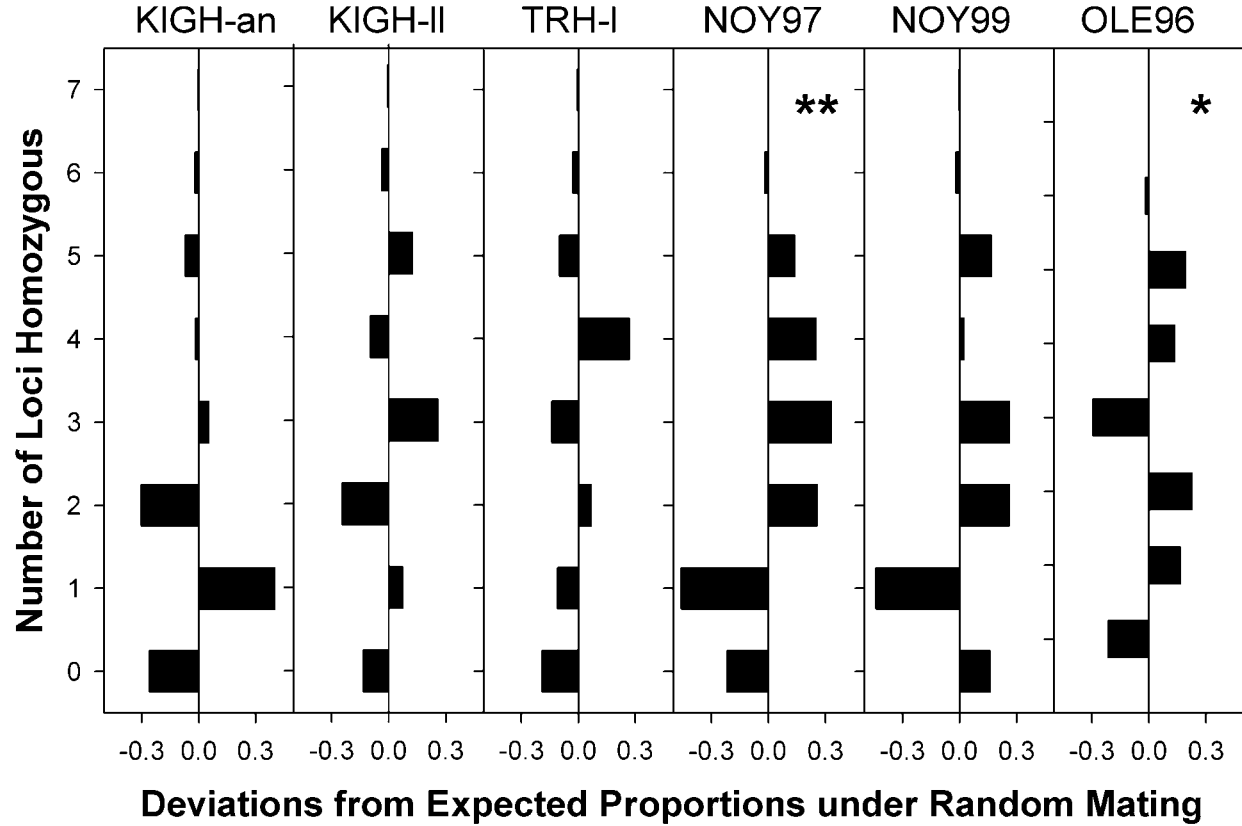
**Table 5.** Fit between observed and expected Mendelian proportions of genotypes at seven microsatellite DNA markers in a full-sib family of 25 juveniles from Green Valley, Russian River.

Locus	Inferred P1 genotype:	Inferred P2 genotype:	F <sub>1</sub> Genotypes	Obs.	Exp.	Total	$\chi^2$	P
<i>Ots-103</i>	224,236	228,232	224,232	5	6.25	25	2.040	0.564
			224,228	4	6.25			
			228,236	8	6.25			
			232,236	8	6.25			
<i>Ots-2</i>	180,184	180,188	180,180	6	6.25	25	3.320	0.345
			180,184	4	6.25			
			180,188	5	6.25			
			184,188	10	6.25			
<i>iso-Ots-2</i>	205,247	213,227	205,213	5	6.25	25	2.040	0.564
			205,227	4	6.25			
			213,247	8	6.25			
			227,247	8	6.25			
<i>Ots-3</i>	145,153	145,157	145,145	8	6	24	1.667	0.644
			145,157	7	6			
			145,153	5	6			
			153,157	4	6			
<i>One-13</i>	197,209	197,219	197,197	10	6.25	25	3.320	0.345
			197,209	5	6.25			
			197,219	6	6.25			
			209,219	4	6.25			
<i>P-53</i>	181,181	173,181	181,181	11	11.5	23	0.861	0.835
			173,181	12	11.5			
<i>Oki-1</i>	092,100	096,112	092,096	9	6	24	3.000	0.392
			092,112	7	6			
			096,100	4	6			
			100,112	4	6			

family sizes within the Green Valley sample, we can estimate the effective number of breeders ( $N_b$ ) in this tributary, following the methods of Hedrick et al. (2000). The estimated  $N_b$  is 10, suggesting that this population is propagated by few adults and may be undergoing rapid genetic drift.



**Fig. 4.** A Neighbor-Joining tree based on allele-sharing among the 59 individuals in the RRGVY98a juvenile sample. Red branches lead to individuals that are not significantly related to any other individual; other colors depict full-sib groups formed by SIBLINGS (see text).



**Fig. 5.** Deviations between observed and expected proportions of individuals in eight multi-loci genotypic categories, from zero through seven microsatellite DNA markers homozygous per individual, for six adult populations with significant  $F_{IS}$  (see Table 7). Expectations are derived from binomial distributions, assuming random mating (see text). Deviations are expressed as the difference between observed and expected numbers divided by the relevant sample size; a square-root transformation (conditional on sign of the deviation) was used to make small deviations visible. Two populations, NOYA97 and OLEA96, show statistically significant deficiencies of individuals with no homozygous loci and excesses of individuals with two to five homozygous loci.

Finally, in addition to the general departures from random mating expectations that we document above, we find significant excesses of multi-loci homozygotes within two of six adult samples examined, NOYA97 and OLEA96 (Fig. 5). This analysis is done on all individuals scored for at least six of the seven markers; individuals are categorized into eight genotypic classes, from individuals homozygous for none of the markers (or heterozygous at all seven markers) to those homozygous for all seven markers (or heterozygous at none of the markers). The expected number of individuals in each category is computed as the product of the probabilities of homozygosity at each locus (from Appendix 1); the probabilities of all possible genotypes are pooled into homozygosity classes and multiplied by the sample size. Significant excesses of individuals homozygous for three to five or six of these highly polymorphic markers in two adult populations suggests that these coho salmon populations are not in random mating equilibrium.

#### Genetic diversity among coho salmon populations

We next test for heterogeneity among samples within 14 drainages or sites in which multiple samples, either spatial or temporal, were collected (Table 6). Heterogeneity is tested by the significance of  $F_{ST}$  among all samples within each drainage or site (indicated by “none” under

the “Sample excluded” column in Table 6. If the initial test is significant (“P-value” < 0.05, Table 6), then samples are removed sequentially, one at a time, with re-testing of the heterogeneity at each step, until a homogeneous pool remains or until all samples are shown to be significantly different from one another (those excluded are tested against each other for homogeneity). Seven pools of homogeneous populations are formed in this manner (underlined in Table 6). Pooling maximizes the sample size within sites and reduces the number of populations for analysis of genetic distance among sites, drainages, and ESUs. The heterogeneity of jacks and older adults in the KIGHA samples suggests significant variance among year classes. The homogeneity of samples from Lagunitas Creek from different year classes and tributaries contrasts with the heterogeneity of samples in other drainages of the Central California ESU.

**Table 6.** Homogeneity of samples within drainages or sites, as determined by sequential exclusion of samples from the initial pool, with re-testing of the significance of  $F_{ST}$  by random permutation of individuals among samples remaining in that pool. Samples are pooled if the significance of  $F_{ST}$  is greater than 0.05.

Drainage, site(s)	pool, if formed	Pool Size	Sample excluded	$F_{ST}$	P-Value
Klamath River, Iron Gate Hatchery		4	None	0.0285	0.000
		3	KIGHA97ll	0.0188	0.000
	<u>Pool: KIGHA97a, KIGHA97nl</u>	<u>2</u>	KIGHA97j	<u>0.0044</u>	<u>0.306</u>
Trinity River, Trinity River Hatchery		2	None	0.0131	0.020
Little River (Humboldt Co.), Little River Delta	<u>pool: LRS00-1, LRS00-2</u>	<u>2</u>	None	<u>0.0031</u>	<u>0.326</u>
South Fork Eel River		4	None	0.0285	0.000
		3	EHOLA97	0.0232	0.000
		2	ESPRS99	0.0088	0.022
Mattole River, Mattole River Delta	<u>pool: MATS98-1, MATS98-2</u>	<u>2</u>	None	<u>0.0048</u>	<u>0.204</u>
Pudding Creek Pudding Creek	<u>pool: PUDY98h, PUDY98k</u>	<u>2</u>	None	<u>-0.0062</u>	<u>0.826</u>
South Fork Noyo, Egg Taking Station		2	None	0.0115	0.000
Albion River, Mainstem and Marsh Creek		2	None	0.0283	0.002
Russian River, Warm Springs Hatchery and Green Valley		7	None	0.0486	0.000
		6	RRGV00	0.0418	0.000
		5	RRGV97	0.0373	0.000
		4	RRGV98b	0.0353	0.000
	<u>pool: RRHA95, RRHA96, RRHY97</u>	<u>3</u>	RRGV98a	<u>0.0089</u>	<u>0.080</u>
Lagunitas Creek, Devils Gulch, San Geronimo, S. G. Arroyo		10	None	0.0124	0.002
	<u>pool: samples from LAG, LDGA, LSG, LSGA</u>	<u>9</u>	LSGAY98	<u>0.0057</u>	<u>0.100</u>
Olema Creek, Mainstem and Blueline		3	None	0.0092	0.000
	<u>pool: OLEA97, OLEY98</u>	<u>2</u>	OLEA96	<u>-0.0001</u>	<u>0.560</u>
Redwood Creek (Marin Co.), Mainstem		2	None	0.0978	0.000
Waddell Creek, Mainstem		2	None	0.0559	0.000
Scott Creek, Hatchery, Mainstem, Upper Fork, Big and Mill Creeks		5	None	0.0170	0.000
		4	SCY99up	0.0134	0.000
		3	SCY99low	0.0094	0.018
	<u>pool: SCA97c, SCA98c</u>	<u>2</u>	SCA95c	<u>0.0021</u>	<u>0.538</u>



After partitioning admixed samples, adjusting the composition of samples having family structure, and then pooling homogeneous samples within sites, we are left with 33 populations for analysis of genetic diversity among populations. The level of departure from random mating expectations remains striking in these samples. Eight samples, including seven adult samples, still show significant  $F_{IS}$  and numerous deviations from random mating genotypic proportions at single loci; five of these samples and 10 others with non-significant  $F_{IS}$  have high levels of linkage disequilibrium ( $LD > 2$ ; Table 7). The frequencies of all alleles observed for each of the seven markers, in each of these 33 populations, are given in Appendix 1, together with observed and expected heterozygosities,  $F_{IS}$  values, and the significance of  $F_{IS}$ .  $F_{ST}$  between pairs of populations within the three ESUs are given in Table 8; all are significant except that between the RRGVY98 samples.

**Table 7.** Deviations from random mating genotypic proportions, by locus (\*,  $P < 0.05$ ; \*\*,  $P < 0.01$ ; \*\*\*,  $P < 0.001$ ) and over all loci ( $F_{IS}$  and associated  $P$ ), and proportion of di-loci pairs showing linkage disequilibrium (LD) for 33 populations of coho salmon formed after adjustment for family structure and pooling of homogeneous samples within drainages.

Population	N	Ots-103	Ots-2	iso-Ots2	Ots-3	One-13	P-53	Oki-1	$F_{IS}$	$P$	LD
KIGHA97an	30								0.061	0.032	1/21
KIGHA97j	15			*					0.019	0.362	4/21
KIGHA97Il	36		*	**		*			0.073	0.028	3/21
TRHA97s	17								0.024	0.266	1/21
TRHA97I	77	***		***				*	0.062	0.004	3/21
LRS00	81		*	*					-0.018	0.818	5/21
EHOLA97	16	*							0.064	0.142	2/21
EREDS97	77			*					0.001	0.452	0/21
EREDA98	22	***							0.056	0.086	2/21
ESPRS99	30		*						-0.057	0.942	3/21
MATS98	48							*	0.017	0.278	2/21
PUDY98	44	*	*						0.067	0.016	5/21
NOYA97	44				**			*	0.064	0.014	1/21
NOYA99	43	*						*	0.076	0.002	2/21
ALBA98	22					***			-0.012	0.598	6/21
ALBY98	16						*	**	0.055	0.106	1/21
RRHA	65								0.025	0.118	8/21
RRGVY97	8							**	-0.032	0.628	0/19
RRGVY98a	25					*			-0.006	0.618	1/21
RRGVY98b	39								-0.049	0.952	7/21
RRGVY00	8							*	-0.257	1.000	0/15
LAG	140					*			0.014	0.186	5/21
LSGAY98	17		*					*	-0.023	0.712	1/21
OLEA96	70				***	*	*	*	0.105	0.000	6/21
OLEA9798	106				*		*	*	0.021	0.142	6/21
RWMA97	15	**		***					0.113	0.120	0/18
RWMY98	24	*							-0.002	0.492	0/21
WADY99lo	31			*					-0.021	0.696	3/21
WADY99up	17						*		-0.085	0.908	2/21
SCA95c	39								-0.051	0.934	1/21
SCA9798c	65	*		***	***		***	**	0.210	0.000	4/21
SCY99low	23								-0.081	0.976	3/21
SCY99up	20								-0.030	0.698	2/21

**Table 8.** Pairwise  $F_{ST}$ , a standardized measure of allele frequency variance between populations, for samples of coho salmon within three geographical regions corresponding to federal and state ESUs (A-C). All values are significant by permutation tests, except for the  $F_{ST}$  between the two 1998 samples of juveniles from Green Valley Creek, Russian River, in panel B.

**A.** Samples of coho salmon from the Southern Oregon / Northern California ESU.

Population	KIGH97j	KIGH97l	TRHA97s	TRHA97l	LRS00	EHOLA97	EREDS97	EREDA98	ESPRS99	MATS98
KIGHA97a	0.025	0.024	0.029	0.036	0.041	0.113	0.097	0.118	0.095	0.112
KIGHA97j		0.047	0.046	0.055	0.030	0.115	0.103	0.118	0.090	0.101
KIGHA97l			0.031	0.021	0.061	0.154	0.129	0.155	0.121	0.141
TRHA97s				0.013	0.054	0.113	0.103	0.122	0.104	0.136
TRHA97l					0.069	0.137	0.126	0.147	0.113	0.145
LRS00						0.083	0.077	0.093	0.077	0.071
EHOLA97							0.038	0.051	0.041	0.064
EREDS97								0.009	0.028	0.063
EREDA98									0.043	0.069
ESPRS99										0.070

**B.** Samples of coho salmon from the Central California ESU.

Population	NOY97	NOY99	ALBA98	ALBY98	RRH	RRGV97	RRGV98a	RRGV98b	RRGV00	LAG	LSGA98	OLE96	OLE9798	RWM97	RWM98
PUDY98	0.028	0.032	0.022	0.011	0.020	0.066	0.068	0.064	0.103	0.017	0.040	0.038	0.033	0.034	0.085
NOYA97		0.012	0.026	0.019	0.009	0.066	0.064	0.065	0.079	0.026	0.041	0.050	0.044	0.042	0.098
NOYA99			0.025	0.027	0.006	0.043	0.079	0.075	0.100	0.019	0.045	0.047	0.035	0.051	0.090
ALBA98				0.028	0.026	0.058	0.092	0.085	0.127	0.026	0.055	0.036	0.026	0.020	0.083
ALBY98					0.020	0.075	0.052	0.051	0.108	0.014	0.033	0.040	0.037	0.063	0.110
RRHA						0.048	0.050	0.048	0.078	0.012	0.030	0.035	0.030	0.042	0.076
RRGVY97							0.079	0.093	0.170	0.053	0.083	0.056	0.048	0.143	0.118
RRGVY98a								0.002	0.113	0.061	0.069	0.057	0.073	0.095	0.146
RRGVY98b									0.096	0.060	0.063	0.060	0.073	0.091	0.142
RRGVY00										0.109	0.101	0.134	0.132	0.160	0.211
LAG											0.027	0.015	0.009	0.053	0.068
LSGAY98												0.040	0.037	0.085	0.093
OLEA96													0.010	0.053	0.101
OLEA9798														0.073	0.064
RWMA97															0.098

**C.** Samples of coho salmon from South of San Francisco, Central California

Population	WADY99u	SCA95c	SCA9798c	SCY99low	SCY99up
WADY99low	0.056	0.014	0.019	0.017	0.046
WADY99up		0.074	0.076	0.041	0.120
SCA95c			0.013	0.017	0.026
SCA9798c				0.020	0.024
SCY99low					0.024